

Replacement Sheet
09/820,788

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1 CCTGCCCTGGT CCTCTGTGCC TGGTGGGGTG GGGGTGCCAG GTGTGTCAG
51 AGGAGCCCAT TTGGTAGTGA GGCAGGTATG GGGCTAGAAG CACTGGTCCC
101 CCTGGCCGTG ATAGTGGCCA TCTTCCTGCT CCTGGTGGAC CTGATGCCACC
151 GGCGCCAACG CTGGCTGCA CGCTACTCAC CAGGCCCCCT GCCACTGCC
201 GGCGCTGGCA ACCTGCTGCA TGTGGACTTC CAGAACACAC CATACTGCTT
251 CGACCAAGTT CGGCAGCGCT TCAGGGACGT GTTCAGCCTG CAGCTGGCCT
301 GGACGCCGGT GGTCGTGCTC AATGGGCTGG CGGCCGTGCG CGAGGGCTG
351 GTGACCCACG GCGAGGACAC CGCCGACCGC CCGCCGTGTC CCATCACCCA
401 GATCCTGGGT TTTGGGCGC GTTCCCAAGG ACGCCCTTT CGCCCCAACG
451 GTCTCTGGGA CAAAGCCGTG AGCAACGTGA TCGCCTCCCT CACCTGCCGG
501 CGCCGCTTCG AGTACGACGA CCCTCGCTTC CTCAGCTGTC TGGAACCTAGC
551 TCAGGAGGGA CTGAAGGAGG AGTCGGGCTT TCTCGCGAG GTGCTGAATG
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751 TGGCAGAGAT GGAGAAGGCC AGGGGAACCTGAGAGCAG CTTCAATGAT
801 GAGAACCTGC GCATAGTGGT GGCTGACCTG TTCTCTGCCG GGATGGTGC
851 CACCTCGACC ACGCTGGCCT GGGGCCCTCT GCTCATGATC CTACATCCGG
901 ATGTGCAGCG CCGGTGCAA CAGGAGATCG ACGACGTGAT AGGGCAGGTG
951 CGGCAGCCAG AGATGGGTGA CCAGGCTCAC ATGCCCTACA CCACTGCCGT
1001 GATTGATGAG GTGAGCGCT TTGGGACAT CGTCCCCCTG GGTGTGACCC
1051 ATATGACATC CCGTGCATC GAAGTACAGG GCTTCCGCAT CCCTAAGGGA
1101 ACACACTCA TCAACCAACCT GTCATCGGTG CTGAAGGATG AGGCCGTCTG
1151 GGAGAACGCC TTCCGCTTCC ACCCCGAACA CTTCTGGAT GCCCAGGGCC
1201 ACTTTGTGAA GCCGGAGGCC TTCTGCCTT TCTCAGCAGG CCGCCGTGCA
1251 TGCCCTGGGG AGCCCTGGC CCGCATGGAG CTCTCCCTCT TCTTCACCTC
1301 CCTGCTGCAG CACTCAGCT TCTCGGTGCC CACTGGACAG CCCCGGCCCA
1351 GCCACCATGG TGTCTTGCT TTCTGGTGA CCCCATCCCC CTATGAGCTT
1401 TGTGCTGTGC CCCGCTAGAA TGGGGTACCT AGTCCCCAGC CTGCTCCCTA
1451 GCCAGAGGCT CTAATGTACA ATAAAGCAAT GTGGTAGTTC CAAAAAA
1501 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA
(SEQ ID NO: 1)

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FEATURES:

5'UTR: 1 - 77
 Start Codon: 78
 Stop Codon: 1416
 3'UTR: 1419

Homologous proteins:

Top 10 BLAST Hits

	Score	E
CRA 18000004889269 /altid=gi 181304 /def=gb AAA53500.1 (M33388...	884	0.0
CRA 18000004927597 /altid=gi 4503223 /def=ref NP_000097.1 cyto...	883	0.0
CRA 18000004923926 /altid=gi 181306 /def=gb AAA35737.1 (M33189...	864	0.0
CRA 18000005007118 /altid=gi 2493367 /def=sp Q29488 CPDH_MACFA ...	827	0.0
CRA 18000005100319 /altid=gi 3913340 /def=sp O18992 CPDJ_CALJA ...	800	0.0
CRA 18000004884804 /altid=gi 486997 /def=pir S37284 cytochrome...	682	0.0
CRA 18000004889271 /altid=gi 522195 /def=gb AAA36403.1 (M24499...	673	0.0
CRA 18000004884803 /altid=gi 461826 /def=sp Q01361 CPDE_BOVIN C...	669	0.0
CRA 18000004939934 /altid=gi 117244 /def=sp P13108 CPD4_RAT CYT...	665	0.0
CRA 18000005107537 /altid=gi 2575863 /def=dbj BAA23125.1 (AB00...	665	0.0

EST:

Sequences producing significant alignments:	Score (bits)	E Value
gi 9872134 /dataset=dbest /taxon=960...	775	0.0
gi 6144331 /dataset=dbest /taxon=9606 ...	648	0.0
gi 6703894 /dataset=dbest /taxon=9606 ...	648	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:

gi|9872134 /liver
 gi|6144331 /kidney
 gi|6703894 /lung

Tissue Expression:

Whole Liver

FIGURE 1

Replacement Sheet
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1 MGLEALVPLA VIVAIPLL V DLMHRRQRWA ARYSPGPLPL PGLGNLLHV
51 FQNTPYCFDQ LRRRGDVFS LQLAWTPVVV LNGLAAVREA LVTHGEDTAD
101 RPPVITQIL GFGPRSQGRP FRPNGLLDKA VSNVIASLTC GRRFEYDDPR
151 FLRLLLDAQE GLKEESGFLR EVLNAPVLL HIPALAGKVL RFQKAFLTQL
201 DELLTEHRMT WDPAQPPRDL TEAFLAEMEK AKGNPESSFN DENLRIVVAD
251 LFSAGMVTT S TTLAWGLLLM ILHPDVQRRV QQEIDDVIGQ VRRPEMDQA
301 HMPYTTAVIH EVQRFGDIVP LGVTMITSRD IEVQGFRIPK GTTLITNLSS
351 VLKDEAVWEK PFRFHPFHFL DAQGHFVKPE AFLPFSAGR ACLGEPLARM
401 ELFLFFTSLL QHFSFSVPTG QPRPSHHGVF AFLVTPSPYE LCAVPR
(SEQ ID NO: 2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

347-350 NLSS

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

327-329 TSR

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 5

1 93-96 THGE
2 198-201 TQLD
3 238-241 SFND
4 327-330 TSRD
5 437-440 SPYE

[4] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 2

1 233-238 GNPESS
2 255-260 GMVTTs

[5] PDOC00009 PS00009 AMIDATION
Amidation site

Number of matches: 2

1 140-143 CGRR
2 387-390 AGRR

[6] PDOC00081 PS00086 CYTOCHROME_P450
Cytochrome P450 cysteine heme-iron ligand signature

385-394 FSAGRRACLG

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	3	23	1.877	Certain
2	68	88	1.096	Certain
3	171	191	0.668	Putative
4	252	272	1.914	Certain
5	400	420	1.402	Certain
6	425	445	0.833	Putative

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BLAST Alignment to Top Hit:

```
>CRA|18000004889269 /altid=gi|181304 /def=gb|AAA53500.1| (M33388)
    cytochrome P450 IID6 [Homo sapiens] /org=Homo sapiens
    /taxon=9606 /dataset=nraa /length=497
    Length = 497

Score = 884 bits (2259), Expect = 0.0
Identities = 444/497 (89%), Positives = 445/497 (89%), Gaps = 51/497 (10%)

Query: 1 MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARYSPGPLPLPGLGNLLHVDFQNTPYCFDQ 60
        MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARY PGPLPLPGLGNLLHVDFQNTPYCFDQ
Sbjct: 1 MGLEALVPLAVIVAIFLLLVDLMHRRQRWAARYPPGPLPLPGLGNLLHVDFQNTPYCFDQ 60

Query: 61 LRRRGDVFSQLAWTPVVVLNGLAARREALVTHGEDTADRPPVPITQILGFGPRSOG-- 118
        LRRRGDVFSQLAWTPVVVLNGLAARREALVTHGEDTADRPPVPITQILGFGPRSOG
Sbjct: 61 LRRRGDVFSQLAWTPVVVLNGLAARREALVTHGEDTADRPPVPITQILGFGPRSQGVF 120

Query: 119 -----RPFRPNGLLDK 129
                    RPFRPNGLLDK
Sbjct: 121 LARYGPAWREQRFSVSTLRNLGLGKSLEQWVTEAAACLCAAFANHSGRPFRPNGLLDK 180

Query: 130 AVSNVIASLTCGRRFEYDDPRFLRLLDQAQEGLKEESGFLREVLNAVAVPVLHIPALAGKV 189
        AVSNVIASLTCGRRFEYDDPRFLRLLDQAQEGLKEESGFLREVLNAVAVPVLHIPALAGKV
Sbjct: 181 AVSNVIASLTCGRRFEYDDPRFLRLLDQAQEGLKEESGFLREVLNAVAVPVLHIPALAGKV 240

Query: 190 LRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFLAEMEAKGNPESSFNDENLRIVVA 249
        LRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFLAEMEAKGNPESSFNDENLRIVVA
Sbjct: 241 LRFQKAFLTQLDELLTEHRMTWDPAQPPRDLTEAFLAEMEAKGNPESSFNDENLRIVVA 300

Query: 250 DLFSAGMVTTSTLAWGLLLMILHPDVQRRVQQEIDDVIGQVRPEMDQAHMPYTTAVI 309
        DLFSAGMVTTSTLAWGLLLMILHPDVQRRVQQEIDDVIGQVRPEMDQAHMPYTTAVI
Sbjct: 301 DLFSAGMVTTSTLAWGLLLMILHPDVQRRVQQEIDDVIGQVRPEMDQAHMPYTTAVI 360

Query: 310 HEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKGTTLITNLSSVLKDEAVWEKPFRHPEHF 369
        HEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKGTTLITNLSSVLKDEAVWEKPFRHPEHF
Sbjct: 361 HEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKGTTLITNLSSVLKDEAVWEKPFRHPEHF 420

Query: 370 LDAQGHFVKPEAFLPFSAGRRACLGEPALARMEFLFFTSLLQHFSFSVPTGQPRPSHHGV 429
        LDAQGHFVKPEAFLPFSAGRRACLGEPALARMEFLFFTSLLQHFSFSVPTGQPRPSHHGV
Sbjct: 421 LDAQGHFVKPEAFLPFSAGRRACLGEPALARMEFLFFTSLLQHFSFSVPTGQPRPSHHGV 480

Query: 430 FAFLVTPSPYELCAVPR 446
        FAFLV+PSPYELCAVPR
Sbjct: 481 FAFLVSPSPYELCAVPR 497 (SEQ ID NO: 4)
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Hmmer search results (Pfam):
Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
PF00067	Cytochrome P450	516.7	1.7e-151	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00067	1/2	35	113 ..	1	92 [.]	78.1	2.7e-21
PF00067	2/2	117	443 ..	150	497 .]	442.7	3.3e-129

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1 AGCCTACAA AGTGCCTGGGA TTACCTGCGT GAGCCACCGG GTCCGGCCTC
51 TTTATGTCTT ACTGTACTGT CTGTCTTGAA AAGTACTTAT TATTTTGAT
101 TGGTCATCA TTTAGTCTAA TAAAATAAG AGTAGTTAC ACACCACAT
151 TACAGTATTA TAATACTCTG TTTTCTG TGCTTACTAT TACCACTGAG
201 TTTTGTACCT TTAGATGATT TCTTCTTGCT CATTAATATC CTTTTTTT
251 TCAGATTGAA AAACCTCCCT TAGCATTCT TGTGGGATAT AGGTCTGGTG
301 TTGATGAAAT CTCCAGCTT TTGTTTGCT GGGAAAGGTCT TTATTCTCC
351 TTCCCTGTTGG AAGGATATTT TTGCCAGATA CGTTATTCTA GGCTAAAAGT
401 TTTTTTCTTC TCAGCACTT AAATATGTCA TGCCACTCCC CCCTGGCCTG
451 TAAGGTTTCC ACTGGAAAGG TGGCTGCCCT ATGTCATGTA TTGGAGCTCT
501 ACTGCATGTT ATTGTTTCT TTTCTTGC TGCTTTAGG ATCCCTTCTT
551 TATCCTGAC CTTTCCGAGT TTAATTATCA GATGCCTGAG GGTGCTCTC
601 TTTGGGTTAA ATCTGCTTGG TGTTCTATAA ACTTCTGTA CAAAAAAATCA
651 GCCAGGCATG GTGGTGGGCA CCTGTAATCC CAGCTACTG GGAGGCTGAG
701 GCAGGAGAAT CGCTTGAACC CTGGAGGTGG AGGTTGCAGT GAGCCAGAT
751 CGCATCATTG CACTCCCAC TGGGCCACAG AGCAAAACTC CGTCTCAAAA
801 AAAAATATTT TTGGGCTCGG TGGTGCCTGT AGTCCCAGCT ACTTGGGAGG
851 CAGGAGGTC CACTGATGTT GAGATTGCAG TGAGCCATGAG TCCTGCCACT
901 GCACTCCGGC CCGGCAACA GAGTGAGACC CTGCTAAAG AAAAATAAAA
951 AATAAAAAG CAACATATCC TAAATAAAGG ATCCCTCATA ATGTTCCAC
1001 CAGATTCTA ATCAGAAACA TGGAGGCCAG GAAGCAGTGG AGAATGACGA
1051 CCCTCAGGCA GCCCTGGAGG ATGCTGTCAC AGGCTGGGC AAGGGCCTC
1101 AGGCCTACCAA CTGGGAGCTC TGGGAACAGC CCTGTTGCAA ACAGGAAGTC
1151 ATGGCCCGGC CAGAGCCAG AATGTGGGCT GAGCTGGGAT CCATGTGACA
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1251 GAAACCTCGG GCATGGCTGG GAAGTGGGGT ACTTGGTCCC GGGTCTGTAT
1301 GTGTGTGTGA CTGGTGTGTG TGAGAGAGAA TGTGTGCCCT GAGTGTCACT
1351 GTGAGTCTGT GTATGTGTGA ATATTGTCTT TGTGTGGGTG ATTTCTGCA
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1451 TGGACAAGAG ATCTGTGCAC CATCAGGTGT GTGCATAGCG TCTGTGCATG
1501 TCAAGAGTGC AAGGTGAAGT GAAGGGACCA GGCCCATGAT GCCACTCATC
1551 ATCAGGAGCT CTAAGGGCCCC AGGTAAGTGC CAGTGACAGA TAAGGGTGCT
1601 GAAGGTCACT CTGGAGTGGG CAGGTGGGG TAGGAAAGG GCAAGGTCAT
1651 GTTCTGGAGG AGGGTTGTG ACTACATTAG GGTGTATGAG CCTAGCTGGG
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1851 AGGACACTCTG GAGCAGGCCA TACCTGCCCT GGCTGACTC TGCCACTGGC
1901 AGCACAGTCACACAGCAG TTCACTCACA GCAGAGGGCG AAGGCCATCA
1951 TCAGCTCCCT TTATAAGGGGA AGGGTCACGC GCTCGGTGTG CCGAGAGTGT
2001 CCTGCCTGGT CCTCTGTGCC TGTTGGGGTG GGGGTGCCAG GTGTGTCCAG
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2101 CCTGGCCATG ATAGTGGCCA TCTTCTGCT CCTGGTGGAC CTGATGCACC
2151 GGCAACAAACG CTGGCTGCA CGCTACCCGC CAGTCCCCT GCCACTGCC
2201 GGGCTGGGC ACCTGTGTC ATGTGGACTT CCAGAACACA CCATACTGCT
2251 TCGACCAAGGT GAGGGAGGAG GTCCCTGGAGG GCGGCAGAGG TCCTGAGGAT
2301 GCCCCAACAC CAGCAACAT GGGTGGTGGG TTAAACACCA GGCTGGATCA
2351 GAAGCCAGGC TGAGAAGGGG AACAGGGTTT GGGGGACGTT CCTGGGAAAG
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2451 GTAGGGCAAG GGCTGGAGG TGGAGCTGGA CTTGGCAGTG GGCATGCAAG
2501 CCCATTGGGC AACATATGTT ATGGAGTACA AAGTCCCTC TGCTGACACC
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2601 AAATCAGCAA ATCGAGGATG AAGGGGGTGC AGTGAACCCGG TTCAAACCTT
2651 TTGCACTGTG GGTCTCTGGG CCTCACTGCT CACCGGCATG GACCATCATC
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2951 TCCCTCTGCA GTTGGCGGC CGCTTGGGG AGCTGTTCAAG CCTGCAGCTG
3001 GCGTGGACGC CGTGGTCGT GCTCAATGGG CTGGCGGCCG TGCGGGAGGC
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3201 GCAGCGCCGA CAGGGCGTGG GGTCTGGAC GTGAACACAGA GATAAAGGCC
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3451 TGGAAAGGTG GTCAAGGGTGG GCAGAGACGA GGTGGGGCCA AACCCGCC
3501 CAGGCAAGGG AGCAATGTGG GTGAGCAAAG AGTGGGCCT GTGCCAGCT

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3551 GGACCGGGCT AGGGACTGCG GGAGACCTT TGGAGGCCA GGGTTGGAGT
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3851 GGAAGGCAGGG GGACGGAGAA GGCAACCCCT TACCCGCATC TCCCCACCCC
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4001 CTTCTCAGG CTGCTGGACC TAGCTCAGGA GGGACTGAAG GAGGAGTCGG
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4101 AGCTCTGAG AGGTGGCGGG GCTGGACTGG GGCCTCCGAA GGGCAGGATT
4151 TGCA TAGATG GGTGGGAA AGGACATTCC AGGAGACCCC ACTGTAAGAA
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4451 AACGCAGAGC ACAGGAGGGAA TTGAGACCCC GTTCTGTCG GTGAGGTGC
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4651 CCTTCCTGGG AAAGAAGGAG AAGGTGAGAG TGGCTGCCAC GGTGGGGGC
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4751 AGGTTGGACC ATGTCATCAC CGCGCGAGGC GCATCTGGC TGACAGGTGC
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4851 CTCGGCCCTG CTCAGGCCAA GGGGAGCCCT GAGAGCAGCT TCAATGATGA
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5151 GGAGAGGTGTC CCCTGGGTGC TGACCCATTG TGGGGACGCA TGTCTGTC
5201 GTCCGTGTCC AACAGGAGAT CGACGACGTG ATAGGGCAGG TGCAGGGACC
5251 AGAGATGGGT GACCAGGCTC ACATGCCCTA CACCACTGCC GTGATTACAG
5301 AGGTGCAGCG CTTGGGGAC ATCATCCCCC TGACTGTGAC CCATATGACA
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6801 GAACATCTCC TGGGAAGGCC CCAGGAAAAC CCAGGACCGA GCCACCC
6851 TCAGCCTGTC ACCTGTGTC CAAATTGGT GGTTCTTGG TCTCACTGAC
6901 TTCAAGAATG AAGCCGTGGA CCCTCACGGT GAGTGTACG GTTCTAAAG
6951 ATGGTGTGTT CAGAGTTGT TCCTTCTGAT GTTAAGACGT GTTCAGAGT
7001 TCTTCCTTCT GGTGGTGCAG TGGTCTTGC GGCTCAGGA GTGAAGCTGC
7051 AGACCTCAC AGTGAAGTGTGTT ACGGCTCTTA AGGCTGCACG TACGGAGTT

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7101 TTCATTCTTC CTGGGGGTT TGTGGTCTCA CTGGCCTCAG GAGTGAACACT
7151 GCAGTCCTTC CAGTGTACA ACTCATAAAAG GCAGTGTGGA CCCAATGAGG
7201 GAGCAGCAGC AGCAAGACTT ACTGCAAACAA GCAAAAGAAT GATGCCAAC
7251 AGGTTGCCGC TGCTACTTCA GGCAGCCTGC TTTTATTCCC TTATCTGACC
7301 CCCACCCACA TCCTGCTGAT TGGCCCATTT TACAGACAGT GGATTGGTCC
7351 ACTTACAGAG AGCTGATTGG TGCAATTACA ATCCCTGAGC TAGACACAGA
7401 GTACTGATTG GTATATTTC AACACCTTGAG CTAGACACAG AGTCTGAAAT
7451 GGTGTATTTA CAACTCCCTTA GCTAGACATA AAGGTTGTC CAGTCCCCAC
7501 TAGATTAGCT AGATAGAGTA GACAGAGAGC ACTGATTGGT GCGTTTACAA
7551 ACCTTGAGTT AGACACAGGG TGCTGACTGG TGTGTTACA AACCTTGAGC
7601 TAGACACAGA GTGCTGATTG GTGTATTTC AATCTTTAG CTAGAAAATAA
7651 AGGTTCCCCA AGTCCCCACC AGATTAGCTA GATAGAGTGC TAATTGGTGC
7701 ATGCACGAAC CGGGAGCTAG ACACAGAGTG CTGATTGGT CATATACAAT
7751 CCTCTGGCTA GACATAAAAG TTCTCCAAGT CCCCACCTGA CTCAGGAGCC
7801 CAGCCAGCTT CGCCTAGTGG ATCCTATGCC AGGGCCACAG GCAGAGCTGC
7851 CTGCTAGTGC CACACCGGGC ACCTGTACTC CTCAGCCCCC GGGCAGTGG
7901 CGGGACCGAG TGCCGTGGAG CAGTGGGAGG CACCCATCCG GGAGGCTCG
7951 GCCTCGCAGG GAGCCCCACCG TAGGGAGGCT TGGGCATGGC AGGCTGCAAG
8001 TCCCTGAGCCC TGCCCCCGGG GGAGGTGACT GAGGCCTGGC GACAATTCAA
8051 GTGTGGTGAG CGCCGGCAGG CCACGAGTAC TGGGGGACCC GGTGCCCCCT
8101 CTGCAGCTGC TGGCCCAGGT GCTAAGCCCC TCACTGCCTG GGGCCAGAGG
8151 CACCAAGCCGG CGCGTCCCGAG TGCAAGGGCCC GCTGAGCCCC TGCCCCACCA
8201 GAACTGGTGC TGCCCCCGCA GCAACCCAGG TTCCCGCACA CGCCTCTCCC
8251 TCCATCACCTC CCCGCAAGCA GACGGAGCCG GCTCCAGCCT CCACCAAGTCC
8301 AGAGAGGGGC TCCCCACAGTG CAGCGCTGGG CTGAACAAGG TCCTAGCCTT
8351 CCAAAAGGCT TTCTGACCC AGCTGGATGA GCTGCTAACT GAGCACAGGA
8401 TGACCTGGGA CCCAGCCCAG CCCCCCCGAG ACCTGACTGA GGCCTTCCT
8451 GGCAGAGATG GAGAAGGTGA GAGTGGCTGC CACGGTGGGG GGCAAGGGTG
8501 GTGGGTGAG CGTCCCAGGA GGAATGAGGG GAGGCTGGC AAAAGGTTGG
8551 ACCAGTGCAT CACCCGGCGA GCGGCATCTG GGCTGACAGG TGCAGAATTG
8601 GAGGTCTATT GGGGGCTACC CGGTTCTGTC CCGAGTATGC TCTCGGCCCT
8651 GCTCAGGCCA AGGGGAACCC TGAGAGCAGC TTCAATGATG AGAACCTGCG
8701 CATAGTGGTG GCTGACCTGT TCTCTGCCGG GATGGTGACC ACCTCGACCA
8751 CGCTGGCTG GGGCCTCTG CTCATGATCC TACATCCGGA TGTGCAGCGT
8801 GAGCCCATCT GGGAAACAGT GCAGGGCCG AGGGAGGAAG GGTACAGGCG
8851 GGGGCCATG AACTTGTG GGACACCCGG GGCTCCAAGC ACAGGCTTGA
8901 CCAGGATCCT GTAAGCCTGA CCTCCTCCAA CATAGGAGGC AAGAAGGAGT
8951 GTCAGGGCCG GACCCCTGG GTGCTGACCC ATTGTGGGGA CGCATGCTG
9001 TCCAGGGCGT GTCCACACAG AGATCGACGA CGTATAGGG CAGGTGGGC
9051 GACCAGAGAT GGGTGACCAAG GCTCACATGC CCTACACCAAC TGCCGTGATT
9101 CATGAGGTGC AGCCCTTGG GGACATCGTC CCCCTGGGTG TGACCCATAT
9151 GACATCCCCTG GACATTCGAA GTACAGGGCT TCCGCATCCC TAAGTAGGC
9201 CTGGGCCNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
9251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
9301 NNNNNNNNCT GCCCAGGGAA CGACACTCAT CACCAACCTG TCATCGGTG
9351 TGAAGGATGA GGGCCTCTGG GAGAAGGCCCT TCCGTTCCA CCCCCAACAC
9401 TTCTGGATG CCCAGGGCCA CTTTGTGAAG CCGGAGGCT TCCGTCCCTT
9451 CTCAGCAGGT GCCTGTGGGG AGCCCGGCTC CCTGTCCCCCT TCCGTGGAGT
9501 CTTGCAGGGG TATCACCCAG GAGCCAGGCT CACTGACGCC CCTCCCCCTCC
9551 CCACAGGCCG CGGTGATGC CTCGGGAGC CCCTGCCCG CATGGAGCTC
9601 TTCTCTTCT TCAACCTCCCT GCTGCGACAC TTCAGCTTCT CGGTGCCAC
9651 TGGACAGCCC CGGGCCAGCC ACCATGGGTG CTTTGCTTTC CTGGTGAGCC
9701 CATCCCCCTA TGACCTTGT GCTGTGCCCC GCTAGAATGG GGTACCTAGT
9751 CCCCCAGCTG CTCCTAGCC AGAGGCTCTA ATGTACAATA AAGCAATGTG
9801 GTAGTCCAA CTGGGTCCC CTGCTCACGC CCTCGTTGGG ATCATCCTCC
9851 TCAGGGCAAC CCCACCCCTG CCTCATTCCCT GCTTACCCCA CCGCCTGGCC
9901 GCATTGAGA CAGGGTACG TTGAGGCTGA GCAGATGTCA GTTACCTTG
9951 CCCATAATCC CATGTCCCCC ACTGACCCAA CTCTGACTGC CCAGATGGT
10001 GACAAGGACT ACATGTCTT GGCATGTGGG GAAGGGGCCA GAATGGGCTG
10051 ACTAGAGGTG TCAGTCAGCC CTGGATGTGG TGGAGAGGGC AGGACTCAGC
10101 CTGGAGGCCC ATATTTCAGG CCTAACTCAG CCCACCCAC ATCAAGGACA
10151 GCAGTCTGC CAGCACCATC ACAACAGTCA CCTCCCTCA TATATGACAC
10201 CCCAAACGG AAGACAAATC ATGGCGTCAG GGAGCTATAT GCCAGGGCTA
10251 CCTACCTCCC AGGGCTAGT CGGCAGGT
(SEQ ID NO: 3)

FEATURES:

Start.....2078
Exon: 2078-2258
Intron: 2259-2961
Exon: 2962-3133

Replacement Sheet
09/820,788

Intron: 3134-3903
 Exon: 3904-4064
 Intron: 4065-4496
 Exon: 4497-4673
 Intron: 4674-4865
 Exon: 4866-5007
 Intron: 5008-5201
 Exon: 5202-5389
 Intron: 5390-5843
 Exon: 5844-5985
 Intron: 5986-9556
 Exon: 9557-9732
 Stop 9733

SNPs:

DNA Position	Major	Minor	Domain	Protein Position		
				Major	Minor	Major
3101	C	T A	Exon	107	T	T T
3439	A	G	Intron			
4908	C	T	Exon	245	P	L
5627	G	A	Intron			
6733	T	C	Intron			
7788	-	C T	Intron			
7867	G	A	Intron			
7948	C	T	Intron			

Context:

DNA Position

3101 GTGTGACCCCCACCCCTGCCCAACGATCAGGAGGCTGGGTCTCCTCCTTCCACCTGCTCA
 CTCCTGGTAGCCCCGGGGTCTGCCAAGGTTCAAATAGGACTAGGACCTGTAGTCTGGGG
 TGATCCTGGCTTGACAAGAGGCCCTGACCCCTCCCTCGCAGTTGGCGCCGCTTCGGGG
 ACGTGTTCAAGCTGCAGCTGGCTGGACGCCGTGGTCGTGCTCAATGGGCTGGCGGGCG
 TCGCGAGGCCATGGTGACCCCGGGCGAGGAACACGCCGACCGCCCGCTCGCCCCATCT

[C, T, A]

CCAGGTCTGGGCTTCGGGGCGCTTCCAAGGCAAGCGGGCGGTGGGGGACAGAGACCGC
 GTTCCGTGGGCCCGGGTGGACAGTGACCGTAGGCCCAGCGCCGACAGGGCGTGGG
 GTCCCTGGACGTGAAACAGAGATAAAGGCCAGCGAGTGGCTGAGGACAGTGGGCCAGAA
 ACCACCTGCACGGGGGAGGTGCGAGTCTGTGGCTGGAGGGGGGGCTACTGCCAG
 ACCGCCAGAACGCCGGTGGCAGGCTGATGCCGAAAGTGGCGTGGCGGGGACCGCG

(nt 2801-3401 of SEQ ID NO: 3)

3439 CGCGGGTGGGGACAGAGACCGCGTTCCGTGGCCCCGGGTGGACAGTGACCGTAGCCC
 AAGCAGCGCCGACAGGGCGTGGGTCTGGACGTGAAACAGAGATAAAGGCCAGCGAGTG
 GGCTGAGGACAGTGGGCCAGGAACCACCTGCACGGGGAGGTGCGAGTCTGTGGCTGG
 GAGGGGGCGGGCTACTGCCAGGCCAGGCCAGGGCTGGCGAGGCTGATGCCGCG
 AAGTGGCGGTGGCGGGGACCGCCCTATGCTGCCGGCTCAGTGTGGCGGGACGGCGGG
 [A, G]
 TCTTCCTTGACTGAAAGGTGGTCAGGGTGGCAGAGACGAGGTGGGGCAAACCCCGCC
 CCAGGCAGGGAGCAATGGGGTGAGCAAAGACTGGGCCCTGCCCCAGCTGGACCGGGC
 TAGGGACTGCGGGAGACCTTGTGGAGGCCAGGGTTGGAGTGGTGGCGAGGGTGGGG
 CAAGGCCCTCATGGCAACGCCAACGTGTCCTGCCGCCAGGGTGATCCTGTCGCG
 TATGGGCCCGGTGGCGAGCAGAGGCCGCTTCCGTGTCACCTGCGCAACTGGGC

(nt 3139-3739 of SEQ ID NO: 3)

4908 ATGACCTGGGACCCAGCCCAGCCACCCCGAGACCTGACTGAGGCCCTCCTGGCAAAGAAG
 GAGAAGGTGAGGTGGCTGCCACCGTGGGGCAAGGGTGGTGAACGTCCAGGA
 GGAATGAGGGGAGGCTGGCAAAGGTTGGACAGTGCATCACCCGGCAGCCGCATCTG
 GGCTGACAGGTGCAAGATTGGAGGTCAATTGGGGCTACCCCGTTATCCCCTGAGTAT
 CCTCTCGGCCCTGCTCAGGCCAACGGGAGCCCTGAGAGCAGCTTCAATGATGAGAACCTG
 [C, T]
 GCATAGTGGTGGGTAACCTGTCCTGCCGGATGGTGGACCACTCGACCGCTGGCCT
 GGGCCCTCTGCTCATGATCCTACACCTGGATGTCAGCGTGAAGCCAGCTGGGCCAA
 GGCAGGGACTGAGGGAGGAAGGGTACAGCTGGGGCCCTGGGCTAGCTGGGACACCCG
 GGGCTTCCACGCCAGGCCAGGCTCTGTAAGCTAACTTCTCCAACACAGGAGG
 AAGGAGAGTGTCCCCCTGGGTGACCCATTGTGGGACGCATGTCAGTCCAGTCCGTG
 (nt 4608-5208 of SEQ ID NO: 3)

Replacement Sheet
09/820,788

5627 CCCCTGAGTGTGACCCATATGACATCCCGTGACATCGAAGTACAGGGCTTCCGATCCCT
AAGGTAGGCCCTGGCGCCCTCCTCACCCCAGCTCAGCACGCACCTGGTGATAGCCCCAG
CATGGCTACTGCCAGGTGGCCACTCTAGGAACCTGGCCACCTAGTCCTCAATGCCAC
CACACTGACTGCCCCACTTGGGTGGGGGTCCAGAGTATAGGCAGGGCTGGCCTGTCCA
TCCAGAGCCCCGTCTAGTGGGAGACAAACCAGGACCTGCCAGAAATGTTGGAGGACCA
[G, A]
CGCCTGCAGGGAGAGGGGGCAGTGTGGGTGCCTCTGAGAGGTGTGACTGCGCCCTGCTGT
GGGGTCGGAGAGGGTACTGTGGAGCTTCCTCGGGCGCAGGACTAGTTGACAGAGTCCAGCT
GTGTGCCAGGCAGTGTGTCCCCGTGTGTTGGCAGGGTCCAGCATCCTAGAG
TCCAGTCCCCACTCTCACCTGCATCTCCTGCCAGGAACGACACTCATCACCAACCTG
TCATCGGTGCTGAAGGATGAGGCCGCTGGGAGAAGCCCTCCGCTTCACCCGAACAC
(nt 5237-5927 of SEQ ID NO: 3)

6733 TGAGACGGGTACGTTGAGGTGAGCAGATGTCAGTTACCCCTGCCATAATCCCATGTCC
CCCACTGACCAACTCTGACTGCCAGATTGGTGACAAGGACTACATTGTCCTGGCATGT
GGGAAGGGGGCAGAATGGCTGACTAGAGGTGTCAGTCAGCCCTGGATGTGGTGGAGAG
GGCAGGACTCACCTGGAGGCCATATTTCAGGCTAACCTCAGCCACCCACATCAGGG
ACAGCAGTCCTGCCAGCACCATCACAAACAGTCACCTCCCTCATATATGACACCCAAAA
[T, C]
GGAAGACAAATCATGTCAGGGAGCTATATGCCAGGGTACCTCCAGGGCTCAGTCGGCA
GGTGCCAGAACATTCCCTGGAAAGGCCAGGAAAACCCAGGACGCCACGCCCTCA
GCTGTCACCTGTGTCAAAATTGGTGGTTCTGGTCTACTGACTTCAGAATGAAG
CCGTGGACCCCTACGGTGAGTTACAGTTCTAAAGATGGTGTTCAGAGTTGTTCC
TTCGTGATGTTAACAGTGTTCAGAGTTCTCCTCTGGTGGTGCGTGGTCTTGTGCC
(nt 6433-7033 of SEQ ID NO: 3)

7788 TCCCAGTCCCCACTAGATTGCTAGATAGAGTAGACAGAGAGCACTGATTGGTGCCTTA
CAAACCTTGAGTTAGACACAGGGTGTGACTGGTGTGTTACAAACCTTGAGCTAGACAC
AGAGTGTGATGGTGATTACAATCTTCTAGAAATAAAGGTTCCCAACTCCCC
ACCAGATTAGCTAGATAGAGTGCTAATTGGTGCATGCACGAAACCCGGAGCTAGACACAGA
GTGCTGATTGGTCATATAACATCCTCTGGCTAGACATAAAAGTTCTCCAAGTCCCCACC
[-, C, T]
GACTCAGGACCCAGCCAGCTCGCTAGTGGATCCTATGCCAGGGCCACAGGCAGAGCT
GCCCTGCTAGTCCCACACCAGGACCTGTACTCCTCAGCCCTGGCAGTGGACGGGACCA
GGTGGCGTGGAGCAGTGGGAGGCACCCATCCGGAGGCTCGGCTCGCAGGGAGCCAC
CGTAGGGAGGCTTGGCATGGCAGGCTGCAAGTCTGAGCCCTGCCGCGGGGAGGTGA
CTGAGGGCTGGCGACAATTCAAGTGTGGTGAAGGCCGCGCAGGCCAGACTGGGGAC
(nt 7488-8088 of SEQ ID NO: 3)

7867 AGGGTGCTGACTGGTGTGTTTACAAACCTTGAGCTAGACACAGAGTGCTGATTGGTGTAT
TTACAATCTTTAGCTAGAAATAAAGGTTCCCAAGTCCCCACCAAGATTAGCTAGATAGA
GTGCTAATTGGTCATGCACGAACCCGGAGCTAGACACAGAGTGCTGATTGGTGCATATA
CAATCCTCTGCTAGACATAAAAGTTCCAACCTCAGGACTCAGGAGCCACGCC
GCTTCGCTACTGGATCCTATGCCAGGGCACAGGCAGAGCTGCCCTGCTAGTCCCCACACC
[G, A]
GGCACCTGTACTCCTCAGCCCTGGGAGTGGACGGGACCAAGGTGGCTGGAGCAGTGG
AGGCACCCATCGGGAGGCTCGGGCTCGCAGGGAGCCACCGTAGGGAGGCTGGCAT
GGCAGGCTGCAAGTCTGAGCCCTGCCCGGGAGGTGACTGAGGCCTGGCGACAATT
CAAGTGTGGTGAAGGCCGAGGCCAGCTACTGGGGACCCGTGCCCTCTGCAGC
TGCTGCCCAAGGTGCTAACGGCCCTACTGCCCTGGGCCAGAGGCACCAAGCCGGCCCTCC
(nt 7567-8167 of SEQ ID NO: 3)

7948 TAAAGGTTCCCCAAGTCCCCACCAAGATTAGCTAGATAGAGTGCTAATTGGTGCATGCACG
AACCCGGAGCTAGACACAGAGTGCTGATTGGTCATATAACATCCTCTGGCTAGACATAA
AAGTTCTCCAAGTCCCCACCTGACTCAGGAGCCACGCCAGCTTCGCTAGTGGATCCTAT
GCCAGGGCCACAGGCAGAGCTGCCCTGCTAGTCCACACCGGGCACCTGACTCCTCAGCC
CTTGGGCAGTGGACGGGACCAAGGTGCCGTGGAGCAGTGGGAGGCACCCATCGGGAGGCT
[C, T]
GGGCCTCGCAGGGAGGCCACCGTAGGGAGGCTTGGGATGGCAGGCTGCAAGTCTGAGC
CCTGCCCGGGAGGTGACTGAGGCCTGGCACAATTCAAGTGTGGTGAAGGCCGCG
GGCAGCAGTACTGGGGACCCGGTGCCCTCTGCAGCTGCTGCCAGGTGCTAAGGCC
CCTCACTGCCCTGGGCCAGAGGCCACGCCGGCCTCCGAGTGCGAGGGCCGCTGAGGCC
CCTGCCCAACCCAGAACTGGTGTGGCCCGCAGCAACCCAGGTTCCCGCACACGCCCTC
(nt 7648-8248 of SEQ ID NO: 3)

Chromosome mapping:
Chromosome #22